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1

SEQUENCE LISTING

<110> ULLRICH, AXEL
GISHIZKY, MIKHAIL
SURES, IRMINGARD

<120> NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

<130> 038602/1260

<140> 09/977,260

<141> 2001-10-16

<150> 08/232,545

<151> 1994-04-22

<160> 24

<170> PatentIn Ver. 2.1

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<211> 2000

<212> DNA

<213> Unknown Organism

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<221> CDS

<222> (258)..(1778)

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<223> Description of Unknown Organism: Megakaryocyte
kinase 1

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aggctcggtc cagtggcacc cagctcccta cctcctgtgc cagccgctg gcctgtggca 180
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tttccctctg gggggcg atg gcg ggg cga ggc tct ctg gtt tcc tgg cgg      290
      Met Ala Gly Arg Gly Ser Leu Val Ser Trp Arg
      1              5              10

gca ttt cac ggc tgt gat tct gct gag gaa ctt ccc cgg gtg agc ccc      338
Ala Phe His Gly Cys Asp Ser Ala Glu Glu Leu Pro Arg Val Ser Pro
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cgc ttc ctc cga gcc tgg cac ccc cct ccc gtc tca gcc agg atg cca      386
Arg Phe Leu Arg Ala Trp His Pro Pro Pro Val Ser Ala Arg Met Pro
      30              35              40

acg agg cgc tgg gcc ccg ggc acc cag tgt atc acc aaa tgc gag cac      434
Thr Arg Arg Trp Ala Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His
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Thr Ile Leu Glu Ala Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His	
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cac acc agt gga cag gag ggg ctg ctg gca gct ggg gcg ctg cgg gag	578
His Thr Ser Gly Gln Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu	
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cgg gag gcc ctc tcc gca gac ccc aag ctc agc ctc atg ccg tgg ttc	626
Arg Glu Ala Leu Ser Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe	
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His Gly Lys Ile Ser Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro	
125 130 135	
gag gat ggg ctg ttc ctg gtg cgg gag tcc gcg cgc cac ccc ggc gac	722
Glu Asp Gly Leu Phe Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp	
140 145 150 155	
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Tyr Val Leu Cys Val Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val	
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Leu His Arg Asp Gly His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys	
175 180 185	
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Asn Leu Met Asp Met Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile	
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tgc acc aag ctg gtg aga cca aag cgg aaa cac ggg acc aag tcg gcc	914
Cys Thr Lys Leu Val Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala	
205 210 215	
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Glu Glu Glu Leu Ala Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu	
220 225 230 235	
aca ttg gga gca cag atc gga gag gga gag ttt gga gct gtc ctg cag	1010
Thr Leu Gly Ala Gln Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln	
240 245 250	
ggt gag tac ctg ggg caa aag gtg gcc gtg aag aat atc aag tgt gat	1058
Gly Glu Tyr Leu Gly Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp	
255 260 265	
gtg aca gcc cag gcc ttc ctg gac gag acg gcc gtc atg acg aag atg	1106
Val Thr Ala Gln Ala Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met	
270 275 280	

caa cac gag aac ctg gtg cgt ctc ctg ggc gtg atc ctg cac cag ggg	1154
Gln His Glu Asn Leu Val Arg Leu Leu Gly Val Ile Leu His Gln Gly	
285 290 295	
ctg tac att gtc atg gag cac gtg agc aag ggc aac ctg gtg aac ttt	1202
Leu Tyr Ile Val Met Glu His Val Ser Lys Gly Asn Leu Val Asn Phe	
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ctg cgg acc cgg ggt cga gcc ctc gtg aac acc gct cag ctc ctg cag	1250
Leu Arg Thr Arg Gly Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln	
320 325 330	
ttt tct ctg cac gtg gcc gag ggc atg gag tac ctg gag agc aag aag	1298
Phe Ser Leu His Val Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys	
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Leu Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp	
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Leu Val Ala Lys Val Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys	
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Gly Leu Asp Ser Ser Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala	
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Leu Lys His Gly Lys Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly	
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Val Leu Leu Trp Glu Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys	
415 420 425	
atg tca ctg aaa gag gtg tcg gag gcc gtg gag aag ggg tac cgc atg	1586
Met Ser Leu Lys Glu Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met	
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Glu Pro Pro Glu Gly Cys Pro Gly Pro Val His Val Leu Met Ser Ser	
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Cys Trp Glu Ala Glu Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala	
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Glu Lys Leu Ala Arg Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val	
480 485 490	
tca ggg cag gac gcc gac ggc tcc acc tcg ccc cga agc cag gag ccc	1778
Ser Gly Gln Asp Ala Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro	
495 500 505	
tgacccacc cgggtggggcc cttggcccca gaggaccgag agagtggaga gtgcggcgtg	1838

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gcaggggctg gcccacgtag ggggctctgg gcgggccgtg gacaccccag acctgcgaag 1958
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<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Megakaryocyte
kinase 1

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Trp His Pro Pro Pro Val Ser Ala Arg Met Pro Thr Arg Arg Trp Ala
35 40 45
Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His Thr Arg Pro Lys Pro
50 55 60
Gly Glu Leu Ala Phe Arg Lys Gly Asp Val Val Thr Ile Leu Glu Ala
65 70 75 80
Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His His Thr Ser Gly Gln
85 90 95
Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu Arg Glu Ala Leu Ser
100 105 110
Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Ser
115 120 125
Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro Glu Asp Gly Leu Phe
130 135 140
Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp Tyr Val Leu Cys Val
145 150 155 160
Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val Leu His Arg Asp Gly
165 170 175
His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys Asn Leu Met Asp Met
180 185 190
Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile Cys Thr Lys Leu Val
195 200 205
Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala Glu Glu Glu Leu Ala
210 215 220

Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu Thr Leu Gly Ala Gln
 225 230 235 240
 Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly
 245 250 255
 Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
 260 265 270
 Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
 275 280 285
 Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met
 290 295 300
 Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
 305 310 315 320
 Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
 325 330 335
 Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
 340 345 350
 Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
 355 360 365
 Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
 370 375 380
 Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
 385 390 395 400
 Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
 405 410 415
 Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu
 420 425 430
 Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly
 435 440 445
 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
 450 455 460
 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
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<213> Unknown Organism

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<222> (82)..(2106)

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<223> Description of Unknown Organism: Megakaryocyte
kinase 2

<400> 3

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                        Met Asp Thr Lys Ser Ile Leu Glu Glu Leu
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ctt ctc aaa aga tca cag caa aag aag aaa atg tca cca aat aat tac 159
Leu Leu Lys Arg Ser Gln Gln Lys Lys Lys Met Ser Pro Asn Asn Tyr
                        15          20          25

aaa gaa cgg ctt ttt gtt ttg acc aaa aca aac ctt tcc tac tat gaa 207
Lys Glu Arg Leu Phe Val Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu
                        30          35          40

tat gac aaa atg aaa agg ggc agc aga aaa gga tcc att gaa att aag 255
Tyr Asp Lys Met Lys Arg Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys
                        45          50          55

aaa atc aga tgt gtg gag aaa gta aat ctc gag gag cag acg cct gta 303
Lys Ile Arg Cys Val Glu Lys Val Asn Leu Glu Glu Gln Thr Pro Val
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gag aga cag tac cca ttt cag att gtc tat aaa gat ggg ctt ctc tat 351
Glu Arg Gln Tyr Pro Phe Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr
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gtc tat gca tca aat gaa gag agc cga agt cag tgg ttg aaa gca tta 399
Val Tyr Ala Ser Asn Glu Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu
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caa aaa gag ata agg ggt aac ccc cac ctg ctg gtc aag tac cat agt 447
Gln Lys Glu Ile Arg Gly Asn Pro His Leu Leu Val Lys Tyr His Ser
                        110          115          120

ggg ttc ttc gtg gac ggg aag ttc ctg tgt tgc cag cag agc tgt aaa 495
Gly Phe Phe Val Asp Gly Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys
                        125          130          135

gca gcc cca gga tgt acc ctc tgg gaa gca tat gct aat ctg cat act 543
Ala Ala Pro Gly Cys Thr Leu Trp Glu Ala Tyr Ala Asn Leu His Thr
                        140          145          150

gca gtc aat gaa gag aaa cac aga gtt ccc acc ttc cca gac aga gtg 591
Ala Val Asn Glu Glu Lys His Arg Val Pro Thr Phe Pro Asp Arg Val
                        155          160          165          170

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Ser Ser Thr Thr Leu Ala Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr	
190 195 200	
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Gly Ser Gln Pro Pro Ser Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser	
205 210 215	
aac tca aag aaa atc tat ggc tcc cag cca aac ttc aac atg cag tat	783
Asn Ser Lys Lys Ile Tyr Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr	
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Ile Pro Arg Glu Asp Phe Pro Asp Trp Trp Gln Val Arg Lys Leu Lys	
235 240 245 250	
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Asn Val Asn His Thr Thr Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser	
270 275 280	
agt tca tct gaa gaa gag gaa aac ctg gat gat tat gac tgg ttt gct	975
Ser Ser Ser Glu Glu Glu Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala	
285 290 295	
ggt aac atc tcc aga tca caa tct gaa cag tta ctc aga caa aag gga	1023
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Lys Glu Gly Ala Phe Met Val Arg Asn Ser Ser Gln Val Gly Met Tyr	
315 320 325 330	
aca gtg tcc tta ttt agt aag gct gtg aat gat aaa aaa gga act gtc	1119
Thr Val Ser Leu Phe Ser Lys Ala Val Asn Asp Lys Lys Gly Thr Val	
335 340 345	
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Lys His Tyr His Val His Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala	
350 355 360	
gaa aac tac tgt ttt gat tcc att cca aag ctt att cat tat cat caa	1215
Glu Asn Tyr Cys Phe Asp Ser Ile Pro Lys Leu Ile His Tyr His Gln	
365 370 375	
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His Asn Ser Ala Gly Met Ile Thr Arg Leu Arg His Pro Val Ser Thr	
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Lys Ala Asn Lys Val Pro Asp Ser Val Ser Leu Gly Asn Gly Ile Trp	
395 400 405 410	
 gaa ctg aaa aga gaa gag att acc ttg ttg aag gag ctg gga agt ggc	1359
Glu Leu Lys Arg Glu Glu Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly	
415 420 425	
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Gln Phe Gly Val Val Gln Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val	
430 435 440	
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Ala Val Lys Met Ile Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Phe	
445 450 455	
 cag gag gcc cag act atg atg aaa ctc agc cat ccc aag ctg gtt aaa	1503
Gln Glu Ala Gln Thr Met Met Lys Leu Ser His Pro Lys Leu Val Lys	
460 465 470	
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Phe Tyr Gly Val Cys Ser Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu	
475 480 485 490	
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Tyr Ile Ser Asn Gly Cys Leu Leu Asn Tyr Leu Arg Ser His Gly Lys	
495 500 505	
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Gly Leu Glu Pro Ser Gln Leu Leu Glu Met Cys Tyr Asp Val Cys Glu	
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525 530 535	
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Ala Arg Asn Cys Leu Val Asp Arg Asp Leu Cys Val Lys Val Ser Asp	
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Phe Gly Met Thr Arg Tyr Val Leu Asp Asp Gln Tyr Val Ser Ser Val	
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Gly Thr Lys Phe Pro Val Lys Trp Ser Ala Pro Glu Val Phe His Tyr	
575 580 585	
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Phe Lys Tyr Ser Ser Lys Ser Asp Val Trp Ala Phe Gly Ile Leu Met	
590 595 600	
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Trp Glu Val Phe Ser Leu Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn	
605 610 615	


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gaa cca ctt cgg gaa aaa gac aag cat tgaagaagaa attaggagt 2126
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atagagactg tgttcatgtg taaagactga gcagaactga aaaattactt attggatatt 2426

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<223> Description of Unknown Organism: Megakaryocyte
kinase 2

<400> 4

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Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu Tyr Asp Lys Met Lys Arg
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Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys Lys Ile Arg Cys Val Glu
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Lys Val Asn Leu Glu Glu Gln Thr Pro Val Glu Arg Gln Tyr Pro Phe
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Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr Val Tyr Ala Ser Asn Glu
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 Asn Pro His Leu Leu Val Lys Tyr His Ser Gly Phe Phe Val Asp Gly
 115 120 125
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 130 135 140
 Leu Trp Glu Ala Tyr Ala Asn Leu His Thr Ala Val Asn Glu Glu Lys
 145 150 155 160
 His Arg Val Pro Thr Phe Pro Asp Arg Val Leu Lys Ile Pro Arg Ala
 165 170 175
 Val Pro Val Leu Lys Met Asp Ala Pro Ser Ser Ser Thr Thr Leu Ala
 180 185 190
 Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr Gly Ser Gln Pro Pro Ser
 195 200 205
 Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser Asn Ser Lys Lys Ile Tyr
 210 215 220
 Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr Ile Pro Arg Glu Asp Phe
 225 230 235 240
 Pro Asp Trp Trp Gln Val Arg Lys Leu Lys Ser Ser Ser Ser Ser Glu
 245 250 255
 Asp Val Ala Ser Ser Asn Gln Lys Glu Arg Asn Val Asn His Thr Thr
 260 265 270
 Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser Ser Ser Ser Glu Glu Glu
 275 280 285
 Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala Gly Asn Ile Ser Arg Ser
 290 295 300
 Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly Lys Glu Gly Ala Phe Met
 305 310 315 320
 Val Arg Asn Ser Ser Gln Val Gly Met Tyr Thr Val Ser Leu Phe Ser
 325 330 335
 Lys Ala Val Asn Asp Lys Lys Gly Thr Val Lys His Tyr His Val His
 340 345 350
 Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala Glu Asn Tyr Cys Phe Asp
 355 360 365
 Ser Ile Pro Lys Leu Ile His Tyr His Gln His Asn Ser Ala Gly Met
 370 375 380
 Ile Thr Arg Leu Arg His Pro Val Ser Thr Lys Ala Asn Lys Val Pro
 385 390 395 400

11

Asp Ser Val Ser Leu Gly Asn Gly Ile Trp Glu Leu Lys Arg Glu Glu
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 Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly Gln Phe Gly Val Val Gln
 420 425 430
 Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val Ala Val Lys Met Ile Lys
 435 440 445
 Glu Gly Ser Met Ser Glu Asp Glu Phe Phe Gln Glu Ala Gln Thr Met
 450 455 460
 Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser
 465 470 475 480
 Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys
 485 490 495
 Leu Leu Asn Tyr Leu Arg Ser His Gly Lys Gly Leu Glu Pro Ser Gln
 500 505 510
 Leu Leu Glu Met Cys Tyr Asp Val Cys Glu Gly Met Ala Phe Leu Glu
 515 520 525
 Ser His Gln Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val
 530 535 540
 Asp Arg Asp Leu Cys Val Lys Val Ser Asp Phe Gly Met Thr Arg Tyr
 545 550 555 560
 Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val
 565 570 575
 Lys Trp Ser Ala Pro Glu Val Phe His Tyr Phe Lys Tyr Ser Ser Lys
 580 585 590
 Ser Asp Val Trp Ala Phe Gly Ile Leu Met Trp Glu Val Phe Ser Leu
 595 600 605
 Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys
 610 615 620
 Val Ser Gln Gly His Arg Leu Tyr Arg Pro His Leu Ala Ser Asp Thr
 625 630 635 640
 Ile Tyr Gln Ile Met Tyr Ser Cys Trp His Glu Leu Pro Glu Lys Arg
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<222> (366)..(1880)

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<223> Description of Unknown Organism: Megakaryocyte
kinase 3

<400> 5

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        1             5             10             15

ctc ccc tgt ttg tcc acg gag gca gac aag tca acc gtg att gaa aat 458
Leu Pro Cys Leu Ser Thr Glu Ala Asp Lys Ser Thr Val Ile Glu Asn
              20             25             30

cca ggg gcc ctt tgc tct ccc cag tca cag agg cat ggc cac tac ttt 506
Pro Gly Ala Leu Cys Ser Pro Gln Ser Gln Arg His Gly His Tyr Phe
              35             40             45

gtg gct ttg ttt gat tac cag gct cgg act gct gag gac ttg agc ttc 554
Val Ala Leu Phe Asp Tyr Gln Ala Arg Thr Ala Glu Asp Leu Ser Phe
              50             55             60

cga gca ggt gac aaa ctt caa gtt ctg gac act ttg cat gag ggc tgg 602
Arg Ala Gly Asp Lys Leu Gln Val Leu Asp Thr Leu His Glu Gly Trp
              65             70             75

tgg ttt gcc aga cac ttg gag aaa aga cga gat ggc tcc agt cag caa 650
Trp Phe Ala Arg His Leu Glu Lys Arg Arg Asp Gly Ser Ser Gln Gln
              80             85             90             95

cta caa ggc tat att cct tct aac tac gtg gct gag gac aga agc cta 698
Leu Gln Gly Tyr Ile Pro Ser Asn Tyr Val Ala Glu Asp Arg Ser Leu
              100            105            110

cag gca gag ccg tgg ttc ttt gga gca atc gga aga tca gat gca gag 746
Gln Ala Glu Pro Trp Phe Phe Gly Ala Ile Gly Arg Ser Asp Ala Glu
              115            120            125

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aaa caa cta tta tat tca gaa aac aag acc ggt tcc ttt cta atc aga	794
Lys Gln Leu Leu Tyr Ser Glu Asn Lys Thr Gly Ser Phe Leu Ile Arg	
130 135 140	
gaa agt gaa agc caa aaa gga gaa ttc tct ctt tca gtt tta gat gga	842
Glu Ser Glu Ser Gln Lys Gly Glu Phe Ser Leu Ser Val Leu Asp Gly	
145 150 155	
gca gtt gta aaa cac tac aga att aaa aga ctg gat gaa ggg gga ttt	890
Ala Val Val Lys His Tyr Arg Ile Lys Arg Leu Asp Glu Gly Gly Phe	
160 165 170 175	
ttt ctc acg cga aga aga atc ttt tca aca ctg aac gaa ttt gtg agc	938
Phe Leu Thr Arg Arg Arg Ile Phe Ser Thr Leu Asn Glu Phe Val Ser	
180 185 190	
cac tac acc aag aca agt gac ggc ctg tgt gtc aag ctg ggg aaa cca	986
His Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val Lys Leu Gly Lys Pro	
195 200 205	
tgc tta aag atc cag gtc cca gct cca ttt gat ttg tcg tat aaa acc	1034
Cys Leu Lys Ile Gln Val Pro Ala Pro Phe Asp Leu Ser Tyr Lys Thr	
210 215 220	
gtg gac caa tgg gag ata gac cgc aac tcc ata cag ctt ctg aag cga	1082
Val Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile Gln Leu Leu Lys Arg	
225 230 235	
ttg gga tct ggt cag ttt ggc gaa gta tgg gaa ggt ctg tgg aac aat	1130
Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Glu Gly Leu Trp Asn Asn	
240 245 250 255	
acc act cca gta gca gtg aaa aca tta aaa cca ggt tca atg gat cca	1178
Thr Thr Pro Val Ala Val Lys Thr Leu Lys Pro Gly Ser Met Asp Pro	
260 265 270	
aat gac ttc ctg agg gag gca cag ata atg aag aac cta aga cat cca	1226
Asn Asp Phe Leu Arg Glu Ala Gln Ile Met Lys Asn Leu Arg His Pro	
275 280 285	
aag ctt atc cag ctt tat gct gtt tgc act tta gaa gat cca att tat	1274
Lys Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu Glu Asp Pro Ile Tyr	
290 295 300	
att att aca gag ttg atg aga cat gga agt ctg caa gaa tat ctc caa	1322
Ile Ile Thr Glu Leu Met Arg His Gly Ser Leu Gln Glu Tyr Leu Gln	
305 310 315	
aat gac act gga tca aaa atc cat ctg act caa cag gta gac atg gcg	1370
Asn Asp Thr Gly Ser Lys Ile His Leu Thr Gln Gln Val Asp Met Ala	
320 325 330 335	
gca cag gtt gcc tct gga atg gcc tat ctg gag tct cgg aac tac att	1418
Ala Gln Val Ala Ser Gly Met Ala Tyr Leu Glu Ser Arg Asn Tyr Ile	
340 345 350	

cac aga gat ctg gct gcc aga aat gtc ctc gtt ggt gaa cat aat atc	1466
His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu His Asn Ile	
355 360 365	
tac aaa gta gca gat ttt gga ctt gcc aga gtt ttt aag gta gat aat	1514
Tyr Lys Val Ala Asp Phe Gly Leu Ala Arg Val Phe Lys Val Asp Asn	
370 375 380	
gaa gac atc tat gaa tct aga cac gaa ata aag ctg ccg gtg aag tgg	1562
Glu Asp Ile Tyr Glu Ser Arg His Glu Ile Lys Leu Pro Val Lys Trp	
385 390 395	
act gcg ccc gaa gcc att cgt agt aat aaa ttc agc att aag tcc gat	1610
Thr Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe Ser Ile Lys Ser Asp	
400 405 410 415	
gta tgg tca ttt gga atc ctt ctt tat gaa atc att act tat ggc aaa	1658
Val Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile Ile Thr Tyr Gly Lys	
420 425 430	
atg cct tac agt ggt atg aca ggt gcc cag gta atc cag atg ttg gct	1706
Met Pro Tyr Ser Gly Met Thr Gly Ala Gln Val Ile Gln Met Leu Ala	
435 440 445	
caa aac tat aga ctt ccg caa cca tcc aac tgt cca cag caa ttt tac	1754
Gln Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys Pro Gln Gln Phe Tyr	
450 455 460	
aac atc atg ttg gag tgc tgg aat gca gag cct aag gaa cga cct aca	1802
Asn Ile Met Leu Glu Cys Trp Asn Ala Glu Pro Lys Glu Arg Pro Thr	
465 470 475	
ttt gag aca ctg cgt tgg aaa ctt gaa gac tat ttt gaa aca gac tct	1850
Phe Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr Phe Glu Thr Asp Ser	
480 485 490 495	
tca tat tca gat gca aat aac ttc ata aga tgaacactgg agaagaatat	1900
Ser Tyr Ser Asp Ala Asn Asn Phe Ile Arg	
500 505	
caaataataa agtagcaaaa caaattcaaa taatccattc caaaatacaa tggtatcaac	1960
caactgcaca atcagtttat cctgacatat tcaagtgata ggataaagtt ggccatgtat	2020
tatgaaaaag attatttgtg cattttattg actgggcaac actgcaggac agtcaaggtc	2080
atatataatt gctcactgcc tggaaaatta agcacactaa accaagttat ttttcttttt	2140
aagagatact tacatttcca tttattgttt gaaatgtcgc gatcaagaga atcaacagat	2200
gatagtccaa tttttactca gtgatgactg tgtagcattt tctgttttac tgattagagt	2260
ggttattcat tattcctcag attgctgaat cccatcaggc tgttattatg aaggaatttg	2320
attgctttgc tgcacagcag gacctgtgct ttgagatttt tttttctctt ttaaaatatc	2380
ctgtaactac aatgatggta aagccatggt aatgacttg attgtacttg gagtaattgc	2440

15

acattttttt ctatgcataa aaaaatgatg cagctgttga gaaaacgaag tctttttcat 2500
 tttgcagaag gaaatgatgg aatttttctg tacttcagta tgtgtcaact gagagtcata 2560
 tacattagtt ttaatctctt aatattgaga atcagggttgc aaaacggatg agttattatc 2620
 tatggaaatg tgagaaatgt ctaatagccc ataaagtctg agaaataggt atcaaaatag 2680
 tttaggaaaa tgagaggaga acagtaggat tgctgtggcc tagacttctg agtaattaat 2740
 aaagaaaaag aagtaccaaa aaaaaaaaaa 2770

<210> 6
 <211> 505
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Megakaryocyte
 kinase 3

<400> 6
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 Pro Cys Leu Ser Thr Glu Ala Asp Lys Ser Thr Val Ile Glu Asn Pro
 20 25 30
 Gly Ala Leu Cys Ser Pro Gln Ser Gln Arg His Gly His Tyr Phe Val
 35 40 45
 Ala Leu Phe Asp Tyr Gln Ala Arg Thr Ala Glu Asp Leu Ser Phe Arg
 50 55 60
 Ala Gly Asp Lys Leu Gln Val Leu Asp Thr Leu His Glu Gly Trp Trp
 65 70 75 80
 Phe Ala Arg His Leu Glu Lys Arg Arg Asp Gly Ser Ser Gln Gln Leu
 85 90 95
 Gln Gly Tyr Ile Pro Ser Asn Tyr Val Ala Glu Asp Arg Ser Leu Gln
 100 105 110
 Ala Glu Pro Trp Phe Phe Gly Ala Ile Gly Arg Ser Asp Ala Glu Lys
 115 120 125
 Gln Leu Leu Tyr Ser Glu Asn Lys Thr Gly Ser Phe Leu Ile Arg Glu
 130 135 140
 Ser Glu Ser Gln Lys Gly Glu Phe Ser Leu Ser Val Leu Asp Gly Ala
 145 150 155 160
 Val Val Lys His Tyr Arg Ile Lys Arg Leu Asp Glu Gly Gly Phe Phe
 165 170 175
 Leu Thr Arg Arg Arg Ile Phe Ser Thr Leu Asn Glu Phe Val Ser His
 180 185 190

Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val Lys Leu Gly Lys Pro Cys
 195 200 205
 Leu Lys Ile Gln Val Pro Ala Pro Phe Asp Leu Ser Tyr Lys Thr Val
 210 215 220
 Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile Gln Leu Leu Lys Arg Leu
 225 230 235 240
 Gly Ser Gly Gln Phe Gly Glu Val Trp Glu Gly Leu Trp Asn Asn Thr
 245 250 255
 Thr Pro Val Ala Val Lys Thr Leu Lys Pro Gly Ser Met Asp Pro Asn
 260 265 270
 Asp Phe Leu Arg Glu Ala Gln Ile Met Lys Asn Leu Arg His Pro Lys
 275 280 285
 Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu Glu Asp Pro Ile Tyr Ile
 290 295 300
 Ile Thr Glu Leu Met Arg His Gly Ser Leu Gln Glu Tyr Leu Gln Asn
 305 310 315 320
 Asp Thr Gly Ser Lys Ile His Leu Thr Gln Gln Val Asp Met Ala Ala
 325 330 335
 Gln Val Ala Ser Gly Met Ala Tyr Leu Glu Ser Arg Asn Tyr Ile His
 340 345 350
 Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu His Asn Ile Tyr
 355 360 365
 Lys Val Ala Asp Phe Gly Leu Ala Arg Val Phe Lys Val Asp Asn Glu
 370 375 380
 Asp Ile Tyr Glu Ser Arg His Glu Ile Lys Leu Pro Val Lys Trp Thr
 385 390 395 400
 Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe Ser Ile Lys Ser Asp Val
 405 410 415
 Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile Ile Thr Tyr Gly Lys Met
 420 425 430
 Pro Tyr Ser Gly Met Thr Gly Ala Gln Val Ile Gln Met Leu Ala Gln
 435 440 445
 Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys Pro Gln Gln Phe Tyr Asn
 450 455 460
 Ile Met Leu Glu Cys Trp Asn Ala Glu Pro Lys Glu Arg Pro Thr Phe
 465 470 475 480
 Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr Phe Glu Thr Asp Ser Ser
 485 490 495

17

Tyr Ser Asp Ala Asn Asn Phe Ile Arg
500 505

<210> 7
<211> 450
<212> PRT
<213> Homo sapiens

<400> 7
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20 25 30
Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
35 40 45
Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
50 55 60
Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
65 70 75 80
Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
85 90 95
Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
100 105 110
Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
115 120 125
Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
130 135 140
Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
145 150 155 160
Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
165 170 175
Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
180 185 190
Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
195 200 205
Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
210 215 220
Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
225 230 235 240
Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
245 250 255

18

Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
 260 265 270
 Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
 275 280 285
 Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
 290 295 300
 Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
 305 310 315 320
 Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
 325 330 335
 Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
 340 345 350
 Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
 355 360 365
 Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
 370 375 380
 Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
 385 390 395 400
 Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
 405 410 415
 Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
 420 425 430
 Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
 435 440 445
 His Leu
 450

<210> 8
 <211> 659
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
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 Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
 20 25 30
 Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
 35 40 45
 Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
 50 55 60

Glu	Thr	Val	Val	Pro	Glu	Lys	Asn	Pro	Pro	Pro	Glu	Arg	Gln	Ile	Pro	65	70	75	80
Arg	Arg	Gly	Glu	Glu	Ser	Ser	Glu	Met	Glu	Gln	Ile	Ser	Ile	Ile	Glu	85	90		95
Arg	Phe	Pro	Tyr	Pro	Phe	Gln	Val	Val	Tyr	Asp	Glu	Gly	Pro	Leu	Tyr	100	105		110
Val	Phe	Ser	Pro	Thr	Glu	Glu	Leu	Arg	Lys	Arg	Trp	Ile	His	Gln	Leu	115	120		125
Lys	Asn	Val	Ile	Arg	Tyr	Asn	Ser	Asp	Leu	Val	Gln	Lys	Tyr	His	Pro	130	135		140
Cys	Phe	Trp	Ile	Asp	Gly	Gln	Tyr	Leu	Cys	Cys	Ser	Gln	Thr	Ala	Lys	145	150		155
Asn	Ala	Met	Gly	Cys	Gln	Ile	Leu	Glu	Asn	Arg	Asn	Gly	Ser	Leu	Lys	165	170		175
Pro	Gly	Ser	Ser	His	Arg	Lys	Thr	Lys	Lys	Pro	Leu	Pro	Pro	Thr	Pro	180	185		190
Glu	Glu	Asp	Gln	Ile	Leu	Lys	Lys	Pro	Leu	Pro	Pro	Glu	Pro	Ala	Ala	195	200		205
Ala	Pro	Val	Ser	Thr	Ser	Glu	Leu	Lys	Lys	Val	Val	Ala	Leu	Tyr	Asp	210	215		220
Tyr	Met	Pro	Met	Asn	Ala	Asn	Asp	Leu	Gln	Leu	Arg	Lys	Gly	Asp	Glu	225	230		235
Tyr	Phe	Ile	Leu	Glu	Glu	Ser	Asn	Leu	Pro	Trp	Trp	Arg	Ala	Arg	Asp	245	250		255
Lys	Asn	Gly	Gln	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Thr	Glu	Ala	260	265		270
Glu	Asp	Ser	Ile	Glu	Met	Tyr	Glu	Trp	Tyr	Ser	Lys	His	Met	Thr	Arg	275	280		285
Ser	Gln	Ala	Glu	Gln	Leu	Leu	Lys	Gln	Glu	Gly	Lys	Glu	Gly	Gly	Phe	290	295		300
Ile	Val	Arg	Asp	Ser	Ser	Lys	Ala	Gly	Lys	Tyr	Thr	Val	Ser	Val	Phe	305	310		315
Ala	Lys	Ser	Thr	Gly	Asp	Pro	Gln	Gly	Val	Ile	Arg	His	Tyr	Val	Val	325	330		335
Cys	Ser	Thr	Pro	Gln	Ser	Gln	Tyr	Tyr	Leu	Ala	Glu	Lys	His	Leu	Phe	340	345		350
Ser	Thr	Ile	Pro	Glu	Leu	Ile	Asn	Tyr	His	Gln	His	Asn	Ser	Ala	Gly	355	360		365

Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
 370 375 380
 Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
 385 390 395 400
 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
 405 410 415
 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
 420 425 430
 Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
 435 440 445
 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
 450 455 460
 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
 465 470 475 480
 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
 485 490 495
 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
 500 505 510
 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
 515 520 525
 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
 530 535 540
 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
 545 550 555 560
 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
 565 570 575
 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
 580 585 590
 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
 595 600 605
 His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu
 610 615 620
 Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu
 625 630 635 640
 Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp
 645 650 655
 Glu Glu Ser

21

<210> 9

<211> 620

<212> PRT

<213> Homo sapiens

<400> 9

Met	Asn	Asn	Phe	Ile	Leu	Leu	Glu	Glu	Gln	Leu	Ile	Lys	Lys	Ser	Gln
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Gln	Lys	Arg	Arg	Thr	Ser	Pro	Ser	Asn	Phe	Lys	Val	Arg	Phe	Phe	Val
			20					25					30		
Leu	Thr	Lys	Ala	Ser	Leu	Ala	Tyr	Phe	Glu	Asp	Arg	His	Gly	Lys	Lys
		35					40					45			
Arg	Thr	Leu	Lys	Gly	Ser	Ile	Glu	Leu	Ser	Arg	Ile	Lys	Cys	Val	Glu
	50					55					60				
Ile	Val	Lys	Ser	Asp	Ile	Ser	Ile	Pro	Cys	His	Tyr	Lys	Tyr	Pro	Phe
65					70					75					80
Gln	Val	Val	His	Asp	Asn	Tyr	Leu	Leu	Tyr	Val	Phe	Ala	Pro	Asp	Arg
				85					90					95	
Glu	Ser	Arg	Gln	Arg	Trp	Val	Leu	Ala	Leu	Lys	Glu	Glu	Thr	Arg	Asn
			100					105					110		
Asn	Asn	Ser	Leu	Val	Pro	Lys	Tyr	His	Pro	Asn	Phe	Trp	Met	Asp	Gly
		115					120					125			
Lys	Trp	Arg	Cys	Cys	Ser	Gln	Leu	Glu	Lys	Leu	Ala	Thr	Gly	Cys	Ala
	130					135					140				
Gln	Tyr	Asp	Pro	Thr	Lys	Asn	Ala	Ser	Lys	Lys	Pro	Leu	Pro	Pro	Thr
145					150					155					160
Pro	Glu	Asp	Asn	Arg	Arg	Pro	Leu	Trp	Glu	Pro	Glu	Glu	Thr	Val	Val
			165						170					175	
Ile	Ala	Leu	Tyr	Asp	Tyr	Gln	Thr	Asn	Asp	Pro	Gln	Glu	Leu	Ala	Leu
		180						185					190		
Arg	Arg	Asn	Glu	Glu	Tyr	Cys	Leu	Leu	Asp	Ser	Ser	Glu	Ile	His	Trp
		195					200					205			
Trp	Arg	Val	Gln	Asp	Arg	Asn	Gly	His	Glu	Gly	Tyr	Val	Pro	Ser	Ser
	210					215					220				
Tyr	Leu	Val	Glu	Lys	Ser	Pro	Asn	Asn	Leu	Glu	Thr	Tyr	Glu	Trp	Tyr
225					230					235					240
Asn	Lys	Ser	Ile	Ser	Arg	Asp	Lys	Ala	Glu	Lys	Leu	Leu	Leu	Asp	Thr
			245						250					255	
Gly	Lys	Glu	Gly	Ala	Phe	Met	Val	Arg	Asp	Ser	Arg	Thr	Ala	Gly	Thr
		260						265					270		

Tyr	Thr	Val	Ser	Val	Phe	Thr	Lys	Ala	Val	Val	Ser	Glu	Asn	Asn	Pro	
		275					280					285				
Cys	Ile	Lys	His	Tyr	His	Ile	Lys	Glu	Thr	Asn	Asp	Asn	Pro	Lys	Arg	
	290					295					300					
Tyr	Tyr	Val	Ala	Glu	Lys	Tyr	Val	Phe	Asp	Ser	Ile	Pro	Leu	Leu	Ile	
305					310					315					320	
Asn	Tyr	His	Gln	His	Asn	Gly	Gly	Gly	Leu	Val	Thr	Arg	Leu	Arg	Tyr	
			325						330					335		
Pro	Val	Cys	Phe	Gly	Arg	Gln	Lys	Ala	Pro	Val	Thr	Ala	Gly	Leu	Arg	
			340					345					350			
Tyr	Gly	Lys	Trp	Val	Ile	Asp	Pro	Ser	Glu	Leu	Thr	Phe	Val	Gln	Glu	
	355						360					365				
Ile	Gly	Ser	Gly	Gln	Phe	Gly	Leu	Val	His	Leu	Gly	Tyr	Trp	Leu	Asn	
	370					375					380					
Lys	Asp	Lys	Val	Ala	Ile	Lys	Thr	Ile	Arg	Glu	Gly	Ala	Met	Ser	Glu	
385					390					395					400	
Glu	Asp	Phe	Ile	Glu	Glu	Ala	Glu	Val	Met	Met	Lys	Leu	Ser	His	Pro	
			405						410					415		
Lys	Leu	Val	Gln	Leu	Tyr	Gly	Val	Cys	Leu	Glu	Gln	Ala	Pro	Ile	Cys	
		420					425						430			
Leu	Val	Phe	Glu	Phe	Met	Glu	His	Gly	Cys	Leu	Ser	Asp	Tyr	Leu	Arg	
		435					440					445				
Thr	Gln	Arg	Gly	Leu	Phe	Ala	Ala	Glu	Thr	Leu	Leu	Gly	Met	Cys	Leu	
	450					455					460					
Asp	Val	Cys	Glu	Gly	Met	Ala	Tyr	Leu	Glu	Glu	Ala	Cys	Val	Ile	His	
465					470					475					480	
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Gln	Val	Ile	
			485					490						495		
Lys	Val	Ser	Asp	Phe	Gly	Met	Thr	Arg	Phe	Val	Leu	Asp	Asp	Gln	Tyr	
		500						505					510			
Thr	Ser	Ser	Thr	Gly	Thr	Lys	Phe	Pro	Val	Lys	Trp	Ala	Ser	Pro	Glu	
		515					520					525				
Val	Phe	Ser	Phe	Ser	Arg	Tyr	Ser	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	
	530					535					540					
Gly	Val	Leu	Met	Trp	Glu	Val	Phe	Ser	Glu	Gly	Lys	Ile	Pro	Tyr	Glu	
545					550					555					560	
Asn	Arg	Ser	Asn	Ser	Glu	Val	Val	Glu	Asp	Ile	Ser	Thr	Gly	Phe	Arg	
			565						570					575		

23

Leu Tyr Lys Pro Arg Leu Ala Ser Thr His Val Tyr Gln Ile Met Asn
 580 585 590

His Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Ala Phe Ser Arg Leu
 595 600 605

Leu Arg Gln Leu Ala Glu Ile Ala Glu Ser Gly Leu
 610 615 620

<210> 10

<211> 527

<212> PRT

<213> Mus sp.

<400> 10

Met Met Val Ser Phe Pro Val Lys Ile Asn Phe His Ser Ser Pro Gln
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Ser Arg Asp Arg Trp Val Lys Lys Leu Lys Glu Glu Ile Lys Asn Asn
 20 25 30

Asn Asn Ile Met Ile Lys Tyr His Pro Lys Phe Trp Ala Asp Gly Ser
 35 40 45

Tyr Gln Cys Cys Arg Gln Thr Glu Lys Leu Ala Pro Gly Cys Glu Lys
 50 55 60

Tyr Asn Leu Phe Glu Ser Ser Ile Arg Lys Thr Leu Pro Pro Ala Pro
 65 70 75 80

Glu Ile Lys Lys Arg Arg Pro Pro Pro Pro Ile Pro Pro Glu Glu Glu
 85 90 95

Asn Thr Glu Glu Ile Val Val Ala Met Tyr Asp Phe Gln Ala Thr Glu
 100 105 110

Ala His Asp Leu Arg Leu Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu
 115 120 125

Lys Asn Asp Leu His Trp Trp Arg Ala Arg Asp Lys Tyr Gly Trp Tyr
 130 135 140

Cys Arg Asn Thr Asn Arg Ser Lys Ala Glu Gln Leu Leu Arg Thr Glu
 145 150 155 160

Asp Lys Glu Gly Gly Phe Met Val Arg Asp Ser Ser Gln Pro Gly Leu
 165 170 175

Tyr Thr Val Ser Leu Tyr Thr Lys Phe Gly Gly Glu Gly Ser Ser Gly
 180 185 190

Phe Arg His Tyr His Ile Lys Glu Thr Ala Thr Ser Pro Lys Lys Tyr
 195 200 205

Tyr Leu Ala Glu Lys His Ala Phe Gly Ser Ile Pro Glu Ile Ile Glu
 210 215 220

Tyr	His	Lys	His	Asn	Ala	Ala	Gly	Leu	Val	Thr	Arg	Leu	Arg	Tyr	Pro	225	230	235	240
Val	Ser	Thr	Lys	Gly	Lys	Asn	Ala	Pro	Thr	Thr	Ala	Gly	Phe	Ser	Tyr	245	250	255	
Asp	Lys	Trp	Glu	Ile	Asn	Pro	Ser	Glu	Leu	Thr	Phe	Met	Arg	Glu	Leu	260	265	270	
Gly	Ser	Gly	Leu	Phe	Gly	Val	Val	Arg	Leu	Gly	Lys	Trp	Arg	Ala	Gln	275	280	285	
Tyr	Lys	Val	Ala	Ile	Lys	Ala	Ile	Arg	Glu	Gly	Ala	Met	Cys	Glu	Glu	290	295	300	
Asp	Phe	Ile	Glu	Glu	Ala	Lys	Val	Met	Met	Lys	Leu	Thr	His	Pro	Lys	305	310	315	320
Leu	Val	Gln	Leu	Tyr	Gly	Val	Cys	Thr	Gln	Gln	Lys	Pro	Ile	Tyr	Ile	325	330	335	
Val	Thr	Glu	Phe	Met	Glu	Arg	Gly	Cys	Leu	Leu	Asn	Phe	Leu	Arg	Gln	340	345	350	
Arg	Gln	Gly	His	Phe	Ser	Arg	Asp	Met	Leu	Leu	Ser	Met	Cys	Gln	Asp	355	360	365	
Val	Cys	Glu	Gly	Met	Glu	Tyr	Leu	Glu	Arg	Asn	Ser	Phe	Ile	His	Arg	370	375	380	
Asp	Leu	Ala	Ala	Arg	Asn	Cys	Leu	Val	Asn	Glu	Ala	Gly	Val	Val	Lys	385	390	395	400
Val	Ser	Asp	Phe	Gly	Met	Ala	Arg	Tyr	Val	Leu	Asp	Asp	Gln	Tyr	Thr	405	410	415	
Ser	Ser	Ser	Gly	Ala	Lys	Phe	Pro	Val	Lys	Trp	Cys	Pro	Pro	Glu	Val	420	425	430	
Phe	Asn	Tyr	Ser	Arg	Phe	Ser	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	435	440	445	
Val	Leu	Met	Trp	Glu	Ile	Phe	Thr	Glu	Gly	Arg	Met	Pro	Phe	Glu	Lys	450	455	460	
Asn	Thr	Asn	Tyr	Glu	Val	Val	Thr	Met	Val	Thr	Arg	Gly	His	Arg	Leu	465	470	475	480
His	Arg	Pro	Lys	Leu	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Val	Met	Leu	Arg	485	490	495	
Cys	Trp	Gln	Glu	Arg	Pro	Glu	Gly	Arg	Pro	Ser	Phe	Glu	Asp	Leu	Leu	500	505	510	
Arg	Thr	Ile	Asp	Glu	Leu	Val	Glu	Cys	Glu	Glu	Thr	Phe	Gly	Arg		515	520	525	

25

<210> 11

<211> 537

<212> PRT

<213> Homo sapiens

<400> 11

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Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
 1              5              10              15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
          20              25              30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
          35              40              45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
          50              55              60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
          65              70              75              80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
          85              90              95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
          100              105              110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
          115              120              125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
          130              135              140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
          145              150              155              160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
          165              170              175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
          180              185              190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
          195              200              205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
          210              215              220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
          225              230              235              240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
          245              250              255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
          260              265              270

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26

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
 275 280 285
 Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
 290 295 300
 Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
 305 310 315 320
 Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
 325 330 335
 Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350
 Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
 355 360 365
 Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
 370 375 380
 Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
 385 390 395 400
 Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
 405 410 415
 Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
 420 425 430
 Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
 435 440 445
 Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
 450 455 460
 Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
 465 470 475 480
 Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
 485 490 495
 Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
 500 505 510
 Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
 515 520 525
 Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 12

<211> 536

<212> PRT

<213> Gallus gallus

<400> 12

Met	Gly	Cys	Val	His	Cys	Lys	Glu	Lys	Ile	Ser	Gly	Lys	Gly	Gln	Gly
1				5					10					15	
Gly	Ser	Gly	Thr	Gly	Thr	Pro	Ala	His	Pro	Pro	Ser	Gln	Tyr	Asp	Pro
			20					25					30		
Asp	Pro	Thr	Gln	Leu	Ser	Gly	Ala	Phe	Thr	His	Ile	Pro	Asp	Phe	Asn
		35					40					45			
Asn	Phe	His	Ala	Ala	Ala	Val	Ser	Pro	Pro	Val	Pro	Phe	Ser	Gly	Pro
	50					55					60				
Gly	Phe	Tyr	Pro	Cys	Asn	Thr	Leu	Gln	Ala	His	Ser	Ser	Ile	Thr	Gly
65					70					75					80
Gly	Gly	Val	Thr	Leu	Phe	Ile	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr
				85					90					95	
Glu	Asp	Asp	Leu	Ser	Phe	Gln	Lys	Gly	Glu	Lys	Phe	His	Ile	Ile	Asn
			100					105					110		
Asn	Thr	Glu	Gly	Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Ser	Ser	Gly	Ala
	115						120					125			
Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile	Gln
	130					135					140				
Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Gly	Arg	Lys	Asp	Ala	Glu	Arg
145					150					155					160
Gln	Leu	Leu	Cys	His	Gly	Asn	Cys	Arg	Gly	Thr	Phe	Leu	Ile	Arg	Glu
				165					170					175	
Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp
			180					185					190		
Glu	Ala	Lys	Gly	Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp
	195						200					205			
Ser	Gly	Gly	Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Ile	Gln
	210					215					220				
Gln	Leu	Val	Gln	His	Tyr	Ile	Glu	Arg	Ala	Ala	Gly	Leu	Cys	Cys	Arg
225					230					235					240
Leu	Ala	Val	Pro	Cys	Pro	Lys	Gly	Thr	Pro	Lys	Leu	Ala	Asp	Leu	Ser
				245					250					255	
Val	Lys	Thr	Lys	Asp	Val	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln	Leu
			260					265					270		
Leu	Gln	Lys	Leu	Gly	Asn	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr
		275					280					285			
Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr
	290					295					300				

28

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
 305 310 315 320
 Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335
 Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
 370 375 380
 Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
 385 390 395 400
 Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
 450 455 460
 Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
 465 470 475 480
 Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
 485 490 495
 Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510
 Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
 515 520 525
 Gln Tyr Gln Pro Gly Asp Asn Gln
 530 535

<210> 13

<211> 536

<212> PRT

<213> Homo sapiens

<400> 13

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
 1 5 10 15
 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
 35 40 45
 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
 50 55 60
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
 290 295 300
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
 305 310 315 320
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

30

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
 370 375 380
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
 385 390 395 400
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
 450 455 460
 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
 465 470 475 480
 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
 485 490 495
 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525
 Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 14
 <211> 543
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
 1 5 10 15
 Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
 20 25 30
 Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
 35 40 45
 Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
 50 55 60

Ser	Ser	Gly	Val	Thr	Pro	Phe	Gly	Gly	Ala	Ser	Ser	Ser	Phe	Ser	Val	65	70	75	80
Val	Pro	Ser	Ser	Tyr	Pro	Ala	Gly	Leu	Thr	Gly	Gly	Val	Thr	Ile	Phe	85	90	95	
Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	Thr	Glu	Asp	Leu	Ser	Phe	100	105	110	
Lys	Lys	Gly	Glu	Arg	Phe	Gln	Ile	Ile	Asn	Asn	Thr	Glu	Gly	Asp	Trp	115	120	125	
Trp	Glu	Ala	Arg	Ser	Ile	Ala	Thr	Gly	Lys	Asn	Gly	Tyr	Ile	Pro	Ser	130	135	140	
Asn	Tyr	Val	Ala	Pro	Ala	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp	Tyr	Phe	145	150	155	160
Gly	Lys	Met	Gly	Arg	Lys	Asp	Ala	Glu	Arg	Leu	Leu	Leu	Asn	Pro	Gly	165	170	175	
Asn	Gln	Arg	Gly	Ile	Phe	Leu	Val	Arg	Glu	Ser	Glu	Thr	Thr	Lys	Gly	180	185	190	
Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Glu	Ile	Arg	Gly	Asp	Asn	195	200	205	
Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	210	215	220	
Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Leu	Gln	Lys	Leu	Val	Lys	His	Tyr	225	230	235	240
Thr	Glu	His	Ala	Asp	Gly	Leu	Cys	His	Lys	Leu	Thr	Thr	Val	Cys	Pro	245	250	255	
Thr	Val	Lys	Pro	Gln	Thr	Gln	Gly	Leu	Ala	Lys	Asp	Ala	Trp	Glu	Ile	260	265	270	
Pro	Arg	Glu	Ser	Leu	Arg	Leu	Glu	Val	Lys	Leu	Gly	Gln	Gly	Cys	Phe	275	280	285	
Gly	Glu	Val	Trp	Met	Gly	Thr	Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Ile	290	295	300	
Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Met	Pro	Glu	Ala	Phe	Leu	Gln	Glu	305	310	315	320
Ala	Gln	Ile	Met	Lys	Lys	Leu	Arg	His	Asp	Lys	Leu	Val	Pro	Leu	Tyr	325	330	335	
Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe	Met	Ser	340	345	350	
Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Glu	Gly	Asp	Gly	Lys	Tyr	Leu	355	360	365	

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Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380
 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400
 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460
 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480
 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495
 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510
 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525
 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535 540

<210> 15
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15
 Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30
 His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
 35 40 45
 His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
 50 55 60
 Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
 65 70 75 80
 Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
 85 90 95

Thr	Phe	Thr	Lys	Gly	Glu	Lys	Phe	His	Ile	Leu	Asn	Asn	Thr	Glu	Gly		
			100					105					110				
Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Ser	Ser	Gly	Lys	Thr	Gly	Cys	Ile		
		115					120					125					
Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp		
		130					135				140						
Tyr	Phe	Gly	Lys	Ile	Gly	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ser		
145					150					155					160		
Pro	Gly	Asn	Pro	Gln	Gly	Ala	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Thr	Thr		
				165					170					175			
Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Gln	Thr	Arg	Gly		
			180					185					190				
Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Met	Gly	Gly	Tyr		
		195					200					205					
Tyr	Ile	Thr	Thr	Arg	Val	Gln	Phe	Asn	Ser	Val	Gln	Glu	Leu	Val	Gln		
	210					215					220						
His	Tyr	Met	Glu	Val	Asn	Asp	Gly	Leu	Cys	Asn	Leu	Leu	Ile	Ala	Pro		
225					230					235					240		
Cys	Thr	Ile	Met	Lys	Pro	Gln	Thr	Leu	Gly	Leu	Ala	Lys	Asp	Ala	Trp		
				245					250					255			
Glu	Ile	Ser	Arg	Ser	Ser	Ile	Thr	Leu	Glu	Arg	Arg	Leu	Gly	Thr	Gly		
			260					265					270				
Cys	Phe	Gly	Asp	Val	Trp	Leu	Gly	Thr	Trp	Asn	Gly	Ser	Thr	Lys	Val		
		275					280					285					
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Pro	Lys	Ala	Phe	Leu		
		290				295					300						
Glu	Glu	Ala	Gln	Val	Met	Lys	Leu	Leu	Arg	His	Asp	Lys	Leu	Val	Gln		
305					310					315					320		
Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe		
				325					330					335			
Met	Cys	His	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Asn	Pro	Glu	Gly	Gln		
			340					345					350				
Asp	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Val	Ala	Glu		
		355					360					365					
Gly	Met	Ala	Tyr	Met	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg		
		370				375					380						
Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Arg	Leu	Ala	Cys	Lys	Ile	Ala	Asp		
385					390					395					400		

Phe	Gly	Leu	Ala	Arg	Leu	Ile	Lys	Asp	Asp	Glu	Tyr	Asn	Pro	Cys	Gln		
				405					410					415			
Gly	Ser	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Phe		
				420					425					430			
Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu		
				435					440					445			
Thr	Glu	Leu	Ile	Thr	Lys	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Asn	Lys		
				450					455					460			
Arg	Glu	Val	Leu	Glu	Gln	Val	Glu	Gln	Gly	Tyr	His	Met	Pro	Cys	Pro		
465					470					475					480		
Pro	Gly	Cys	Pro	Ala	Ser	Leu	Tyr	Glu	Ala	Met	Glu	Gln	Thr	Trp	Arg		
				485					490					495			
Leu	Asp	Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu		
				500					505					510			
Glu	Asp	Tyr	Phe	Thr	Ser	Ala	Glu	Pro	Gln	Tyr	Gln	Pro	Gly	Asp	Gln		
				515					520					525			

Thr

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<210> 16
<211> 512
<212> PRT
<213> Homo sapiens
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<400> 16																
Met	Gly	Cys	Ile	Lys	Ser	Lys	Gly	Lys	Asp	Ser	Leu	Ser	Asp	Asp	Gly	
1				5					10					15		
Val	Asp	Leu	Lys	Thr	Gln	Pro	Val	Arg	Asn	Thr	Glu	Arg	Thr	Ile	Tyr	
			20					25					30			
Val	Arg	Asp	Pro	Thr	Ser	Asn	Lys	Gln	Gln	Arg	Pro	Val	Pro	Glu	Ser	
		35					40					45				
Gln	Leu	Leu	Pro	Gly	Gln	Arg	Phe	Gln	Thr	Lys	Asp	Pro	Glu	Glu	Gln	
	50					55					60					
Gly	Asp	Ile	Val	Val	Ala	Leu	Tyr	Pro	Tyr	Asp	Gly	Ile	His	Pro	Asp	
65					70					75					80	
Asp	Leu	Ser	Phe	Lys	Lys	Gly	Glu	Lys	Met	Lys	Val	Leu	Glu	Glu	His	
				85					90					95		
Gly	Glu	Trp	Trp	Lys	Ala	Lys	Ser	Leu	Leu	Thr	Lys	Lys	Glu	Gly	Phe	
			100					105					110			
Ile	Pro	Ser	Asn	Tyr	Val	Ala	Lys	Leu	Asn	Thr	Leu	Glu	Thr	Glu	Glu	
		115					120					125				

Trp	Phe	Phe	Lys	Asp	Ile	Thr	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu
130						135					140				
Ala	Pro	Gly	Asn	Ser	Ala	Gly	Ala	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Thr
145					150					155					160
Leu	Lys	Gly	Ser	Phe	Ser	Leu	Ser	Val	Arg	Asp	Phe	Asp	Pro	Val	His
				165					170					175	
Gly	Asp	Val	Ile	Lys	His	Tyr	Lys	Ile	Arg	Ser	Leu	Asp	Asn	Gly	Gly
			180					185					190		
Tyr	Tyr	Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Cys	Ile	Ser	Asp	Met	Ile
		195					200					205			
Lys	His	Tyr	Gln	Lys	Gln	Ala	Asp	Gly	Leu	Cys	Arg	Arg	Leu	Glu	Lys
	210					215					220				
Ala	Cys	Ile	Ser	Pro	Lys	Pro	Gln	Lys	Pro	Trp	Asp	Lys	Asp	Ala	Trp
225					230					235					240
Glu	Ile	Pro	Arg	Glu	Ser	Ile	Lys	Leu	Val	Lys	Arg	Leu	Gly	Ala	Gly
				245					250					255	
Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Asn	Ser	Thr	Lys	Val
			260					265					270		
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Val	Gln	Ala	Phe	Leu
		275					280					285			
Glu	Glu	Ala	Asn	Leu	Met	Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Arg
	290					295					300				
Leu	Tyr	Ala	Val	Val	Thr	Arg	Glu	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu
305					310					315					320
Tyr	Met	Ala	Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly
				325					330					335	
Gly	Lys	Val	Leu	Leu	Pro	Lys	Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala
			340					345					350		
Glu	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Lys	Asn	Tyr	Ile	His	Arg	Asp	Leu
		355					360					365			
Arg	Ala	Ala	Asn	Val	Leu	Val	Ser	Glu	Ser	Leu	Met	Cys	Lys	Ile	Ala
	370					375					380				
Asp	Phe	Gly	Leu	Ala	Arg	Val	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg
385					390					395					400
Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn
				405					410					415	
Phe	Gly	Cys	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu
			420					425					430		

Leu	Tyr	Glu	Ile	Val	Thr	Tyr	Gly	Lys	Ile	Pro	Tyr	Pro	Gly	Arg	Thr
435						440						445			
Asn	Ala	Asp	Val	Met	Thr	Ala	Leu	Ser	Gln	Gly	Tyr	Arg	Met	Pro	Arg
450						455						460			
Val	Glu	Asn	Cys	Pro	Asp	Glu	Leu	Tyr	Asp	Ile	Met	Lys	Met	Cys	Trp
465						470						475			480
Lys	Glu	Lys	Ala	Glu	Glu	Arg	Pro	Thr	Phe	Asp	Tyr	Leu	Gln	Ser	Val
			485						490						495
Leu	Asp	Asp	Phe	Tyr	Thr	Ala	Thr	Glu	Gly	Gln	Tyr	Gln	Gln	Gln	Pro
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<211> 505
<212> PRT
<213> Homo sapiens
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Ser	Lys	Thr	Glu	Thr	Ser	Ala	Ser	Pro	His	Cys	Pro	Val	Tyr	Val	Pro		
				20		25				30							
Asp	Pro	Thr	Ser	Thr	Ile	Lys	Pro	Gly	Pro	Asn	Ser	His	Asn	Ser	Asn		
35				40				45									
Thr	Pro	Gly	Ile	Arg	Glu	Ala	Gly	Ser	Glu	Asp	Ile	Ile	Val	Val	Ala		
50				55				60									
Leu	Tyr	Asp	Tyr	Glu	Ala	Ile	His	His	Glu	Asp	Leu	Ser	Phe	Gln	Lys		
65				70				75					80				
Gly	Asp	Gln	Met	Val	Val	Leu	Glu	Glu	Ser	Gly	Glu	Trp	Trp	Lys	Ala		
				85		90				95							
Arg	Ser	Leu	Ala	Thr	Arg	Lys	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val		
100				105				110									
Ala	Arg	Val	Asp	Ser	Leu	Glu	Thr	Glu	Glu	Trp	Phe	Phe	Lys	Gly	Ile		
115				120				125									
Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro	Gly	Asn	Met	Leu		
130				135				140									
Gly	Ser	Phe	Met	Ile	Arg	Asp	Ser	Glu	Thr	Thr	Lys	Gly	Ser	Tyr	Ser		
145				150				155					160				
Leu	Ser	Val	Arg	Asp	Tyr	Asp	Pro	Arg	Gln	Gly	Asp	Thr	Val	Lys	His		
				165		170				175							
Tyr	Lys	Ile	Arg	Thr	Leu	Asp	Asn	Gly	Gly	Phe	Tyr	Ile	Ser	Pro	Arg		
180				185				190									

Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly
 195 200 205
 Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys
 210 215 220
 Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser
 225 230 235 240
 Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp
 245 250 255
 Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys
 260 265 270
 Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met
 275 280 285
 Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr
 290 295 300
 Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu
 305 310 315 320
 Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys
 325 330 335
 Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu
 340 345 350
 Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365
 Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val
 370 375 380
 Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile
 385 390 395 400
 Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys
 405 410 415
 Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr
 420 425 430
 Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala
 435 440 445
 Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu
 450 455 460
 Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg
 465 470 475 480
 Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala
 485 490 495

38

Thr Glu Ser Gln Tyr Gln Gln Gln Pro
 500 505

<210> 18
 <211> 509
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
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 Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
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 Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
 35 40 45
 Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
 50 55 60
 Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
 65 70 75 80
 Gly Phe Glu Lys Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu
 85 90 95
 Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
 100 105 110
 Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
 115 120 125
 Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
 130 135 140
 Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
 145 150 155 160
 Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
 165 170 175
 Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
 180 185 190
 Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
 195 200 205
 Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
 210 215 220
 Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
 225 230 235 240
 Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe
 245 250 255

39

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val
 260 265 270
 Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu
 275 280 285
 Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr
 290 295 300
 Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu
 305 310 315 320
 Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu
 325 330 335
 Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met
 340 345 350
 Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 355 360 365
 Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly
 370 375 380
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 385 390 395 400
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr
 405 410 415
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu
 420 425 430
 Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu
 435 440 445
 Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn
 450 455 460
 Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg
 465 470 475 480
 Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
 485 490 495
 Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro
 500 505

<210> 19
 <211> 499
 <212> PRT
 <213> Mus sp.

<400> 19
 Met Gly Leu Leu Ser Ser Lys Arg Gln Val Ser Glu Lys Gly Lys Gly
 1 5 10 15

Trp	Ser	Pro	Val 20	Lys	Ile	Arg	Thr	Gln 25	Asp	Lys	Ala	Pro	Pro	Pro	Leu
Pro	Pro	Leu 35	Val	Val	Phe	Asn	His 40	Leu	Ala	Pro	Pro	Ser 45	Pro	Asn	Gln
Asp	Pro	Asp 50	Glu	Glu	Glu	Arg 55	Phe	Val	Val	Ala	Leu 60	Phe	Asp	Tyr	Ala
Ala	Val	Asn 65	Asp	Arg	Asp 70	Leu	Gln	Val	Leu	Lys 75	Gly	Glu	Lys	Leu	Gln 80
Val	Leu	Arg	Ser	Thr 85	Gly	Asp	Trp	Trp	Leu 90	Ala	Arg	Ser	Leu	Val 95	Thr
Gly	Arg	Glu	Gly 100	Tyr	Val	Pro	Ser	Asn 105	Phe	Val	Ala	Pro	Val	Glu	Thr
Leu	Glu	Val 115	Glu	Lys	Trp	Phe	Phe 120	Arg	Thr	Ile	Ser	Arg 125	Lys	Asp	Ala
Glu	Arg	Gln 130	Leu	Leu	Ala 135	Pro	Met	Asn	Lys	Ala	Gly 140	Ser	Phe	Leu	Ile
Arg	Glu	Ser 145	Glu	Ser	Asn 150	Lys	Gly	Ala	Phe	Ser 155	Leu	Ser	Val	Lys	Asp 160
Ile	Thr	Thr	Gln	Gly 165	Glu	Val	Val	Lys	His 170	Tyr	Lys	Ile	Arg	Ser 175	Leu
Asp	Asn	Gly 180	Gly	Tyr	Tyr	Ile	Ser	Pro 185	Arg	Ile	Thr	Phe	Pro	Thr	Leu
Gln	Ala	Leu 195	Val	Gln	His	Tyr	Ser 200	Lys	Lys	Gly	Asp 205	Gly	Leu	Cys	Gln
Lys	Leu	Thr 210	Leu	Pro	Cys	Val 215	Asn	Leu	Ala	Pro	Lys 220	Asn	Leu	Trp	Ala
Gln	Asp	Glu 225	Trp	Glu	Ile 230	Pro	Arg	Gln	Ser	Leu 235	Lys	Leu	Val	Arg	Lys 240
Leu	Gly	Ser	Gly	Gln 245	Phe	Gly	Glu	Val	Trp 250	Met	Gly	Tyr	Tyr	Lys	Asn 255
Asn	Met	Lys 260	Val	Ala	Ile	Lys	Thr	Leu 265	Lys	Glu	Gly	Thr	Met	Ser	Pro
Glu	Ala	Phe 275	Leu	Gly	Glu	Ala	Asn 280	Val	Met	Lys	Thr	Leu 285	Gln	His	Glu
Arg	Leu	Val 290	Arg	Leu	Tyr	Ala 295	Val	Val	Thr	Arg	Glu 300	Pro	Ile	Tyr	Ile
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<212> DNA
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<223> A, T, C, G, other or unknown

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<221> modified base
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<223> A, T, C, G, other or unknown
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42

<222> (26)

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<223> Description of Artificial Sequence: Primer

<400> 20

ggaattccca ymgncrayytn rcnrcnmg

28

<210> 21

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> A, T, C, G, other or unknown

<220>

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<223> A, T, C, G, other or unknown

<220>

<221> modified_base

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<223> A, T, C, G, other or unknown

<220>

<223> Description of Artificial Sequence: Primer

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ggaattccrw rnswwcanac stcnsa

26

<210> 22

<211> 15

<212> PRT

<213> Artificial Sequence

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peptide

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<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

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Gln Gln Leu Leu Ser Ser Ile Glu Pro Leu Arg Glu Lys Asp Lys His
1 5 10 15

<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative
peptide

<220>

<221> MOD_RES

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<223> Variable amino acid

<400> 24

Ser Asp Val Trp Ser Xaa
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